

FIGURE 1

GENOMIC ALIGNMENT

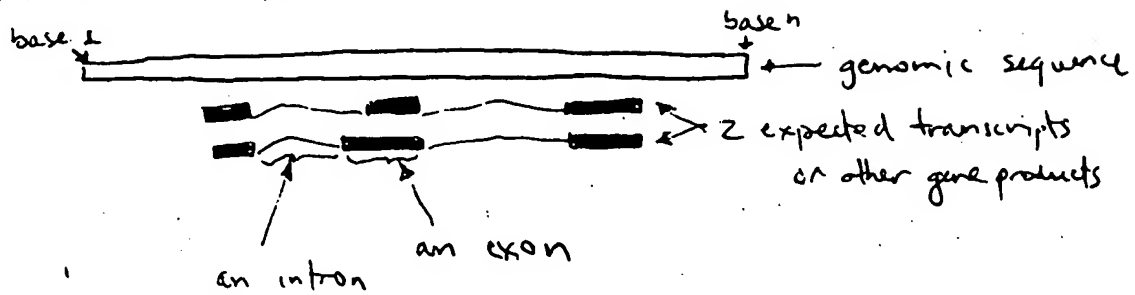


FIGURE 2

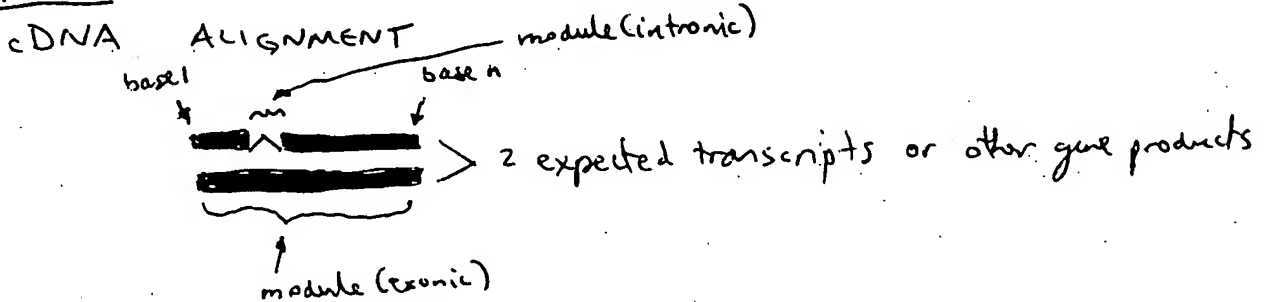
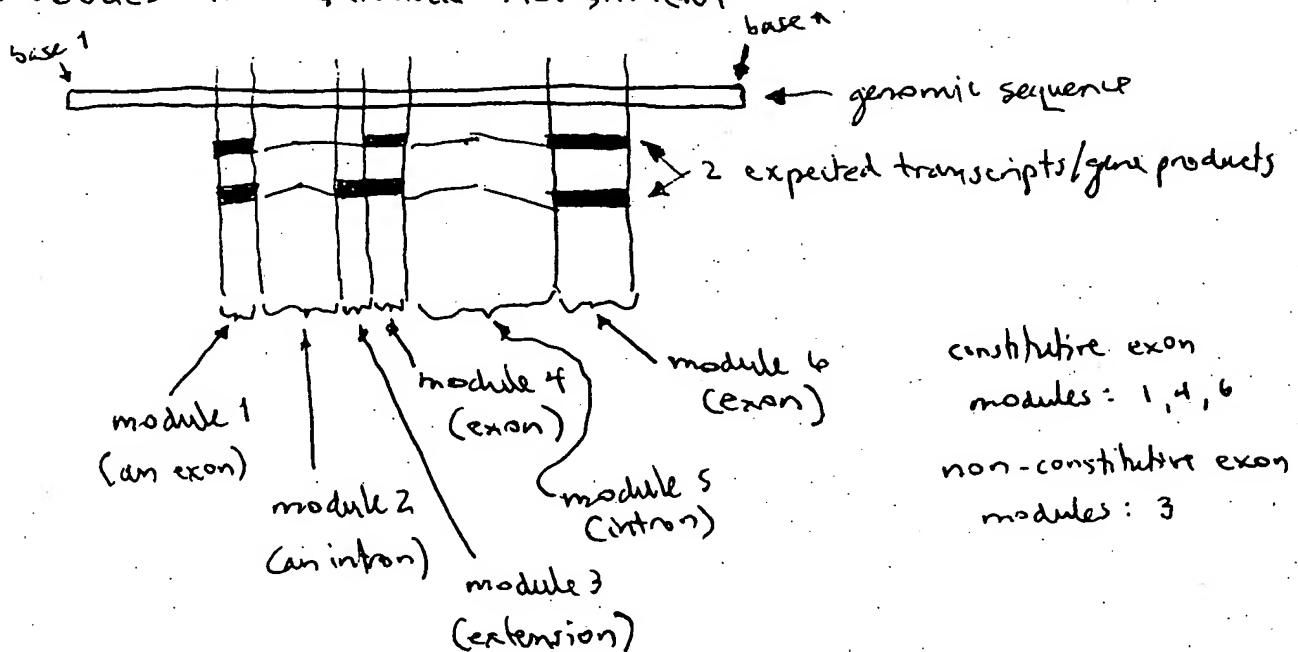


FIGURE 3

MODULES IN GENOMIC ALIGNMENT

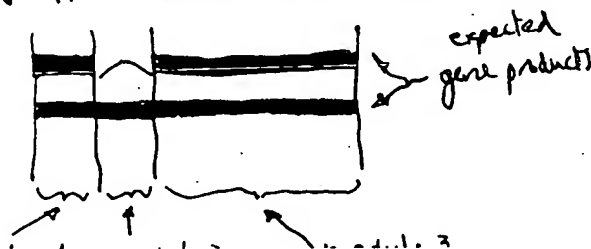


constitutive exon
modules: 1, 4, 6

non-constitutive exon
modules: 3

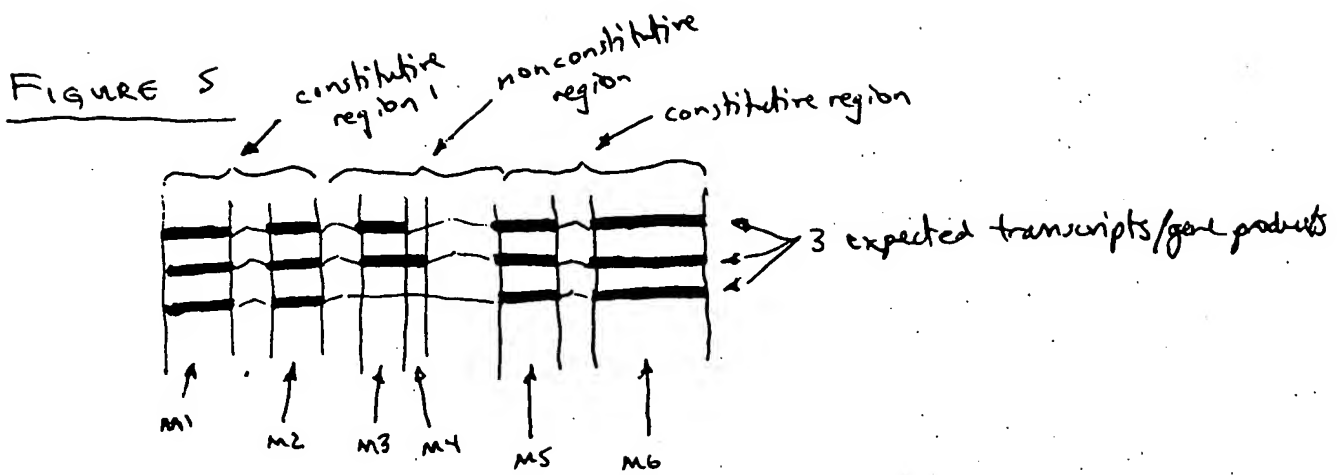
FIGURE 4

MODULES IN cDNA ALIGNMENT



constitutive modules: 1, 3

non constitutive modules: 2



M1 to M6 are exon modules. (Intron modules omitted.)

Constitutive modules: 1, 2, 5, 6

Nonconstitutive modules: 3, 4

Groups of adjacent constitutive modules: (1, 2), (5, 6)

Groups of adjacent nonconstitutive modules: (3, 4)

Figure 6

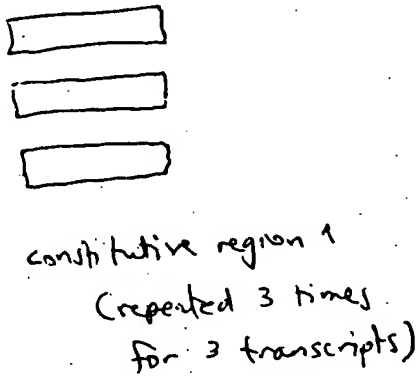
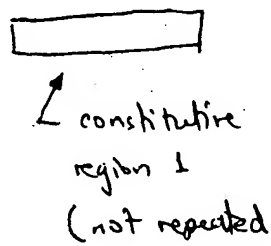
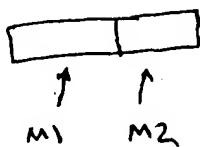


Figure 7



Constitutive region 1

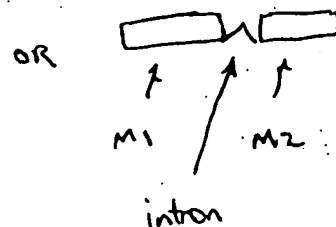


Figure 8

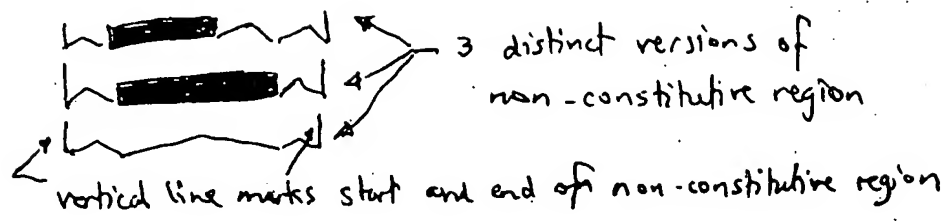
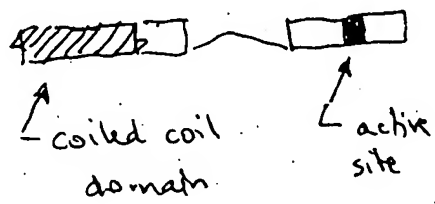


Figure 9



Example of domain annotation

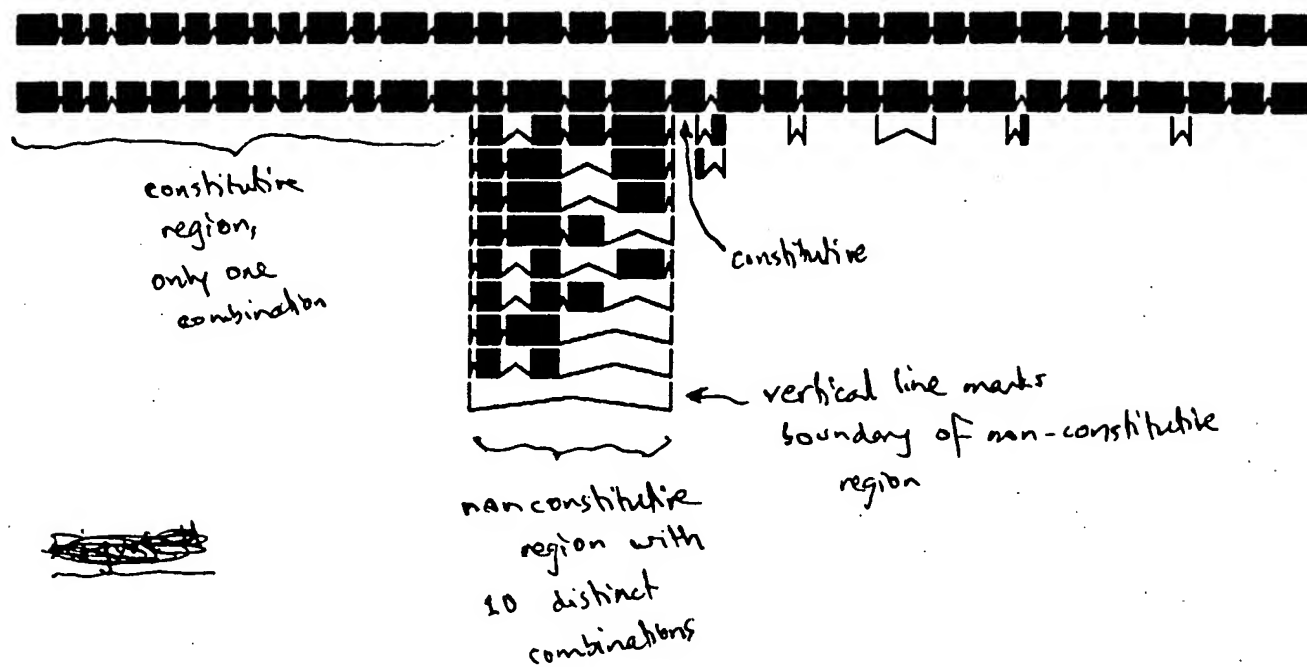
ZC1 Figure 10

Figure 11

An EST (in orange), aligned against all transcripts (in blue) of AKT3 in the NCBI human genome annotations. The EST contains an additional exon not present in the transcripts.

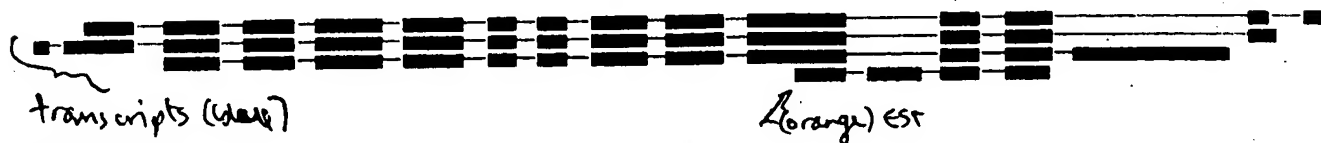
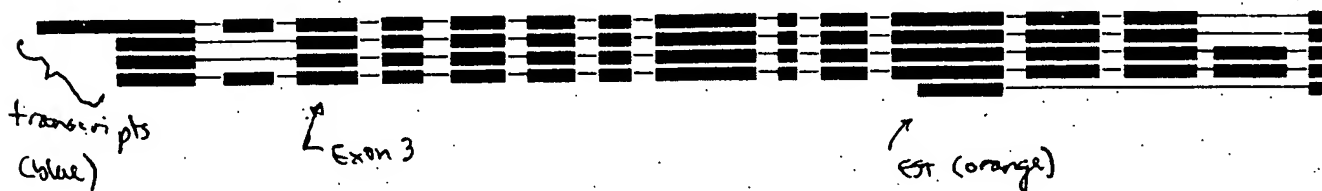


Figure 12

An EST (in orange), aligned against all transcripts (in blue) of the kinase GPRK2L in the NCBI human genome annotations. The EST is missing 2 or 3 exons present in the transcripts.



To "zoom in" on exon 3, the scale for that region can be altered while retaining the same scale for the rest of the view. The graphic representation of the selected region can be altered as a function of the scale. E.g., at a certain scale, the bar could be replaced with the NT or AA sequence.

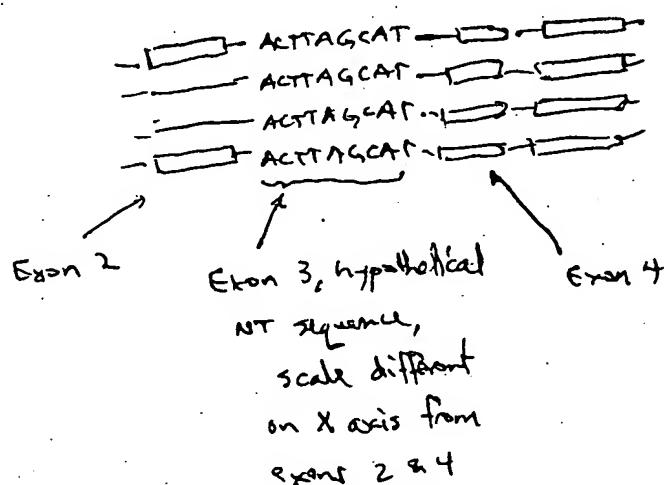


Figure 3

The sequences of Figure 1, as displayed using a single base scale for all introns and exons. Note that it is impossible to determine the relative lengths of exons from the graphics alone. In Figure 1, exons are displayed using one linear scale, while introns are displayed as $\log(\text{length})$.

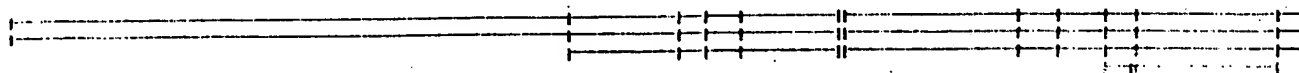


Figure 4

The sequences of Figure 2, as displayed using a single base scale for all introns and exons.

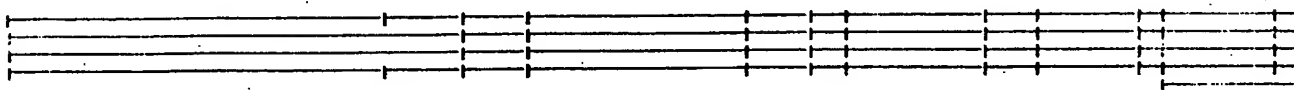
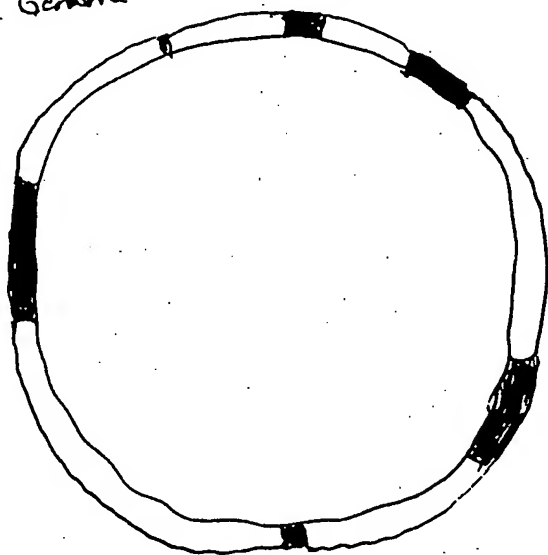


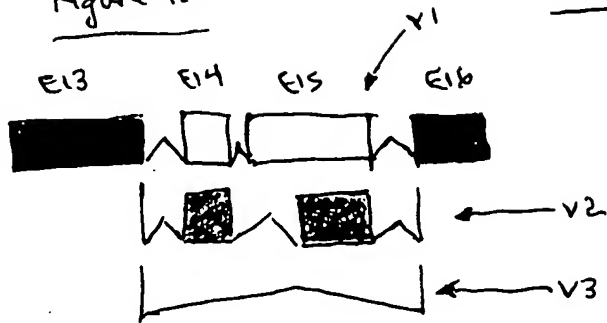
Figure 15

Bacterial Genome



Regions in black are displayed using one scale, while regions in white are displayed in another. The effect is to alter the relative sizes of the arcs allocated to different annotations.

Figure 16

Expression Levels in a Splice Graph

Exons 13 through 16 of gene ZC1. Three alternately spliced forms are depicted across the region comprising exons 14 and 15. Exons 13 and 16 are filled with solid black, indicating one expression level, equal to the gene expression. The alternately spliced forms, labeled V1, V2, and V3, must each have an expression level less than or equal to the gene expression. In the figure, V1 (variant one) is filled with white (fully desaturated) to indicate an expression level of zero (not expressed). Variant two (V2) is filled with gray (partial saturation of the color black) to indicate expression greater than zero but less than the gene expression level. By inference, variant three (V3) accounts for the remainder of the expression. Its expression level could be displayed by a solid shape filled with gray.

Figure 17

Expression Levels in a Genome Browser

Variant one (V1) is not expressed, while variants two and three (V2 & V3) are expressed in approximately equal quantities. white = not expressed. black = gene expression.

Figure 18 Other methods of Indicating Expression Level

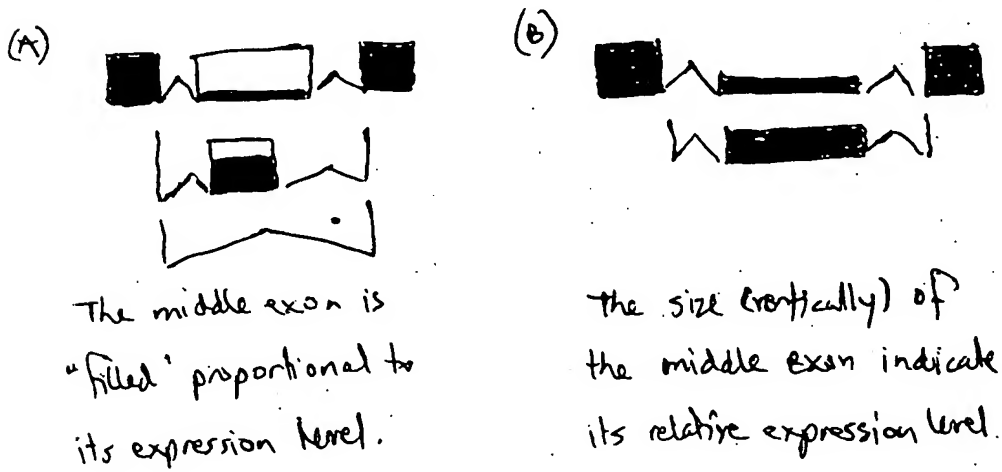
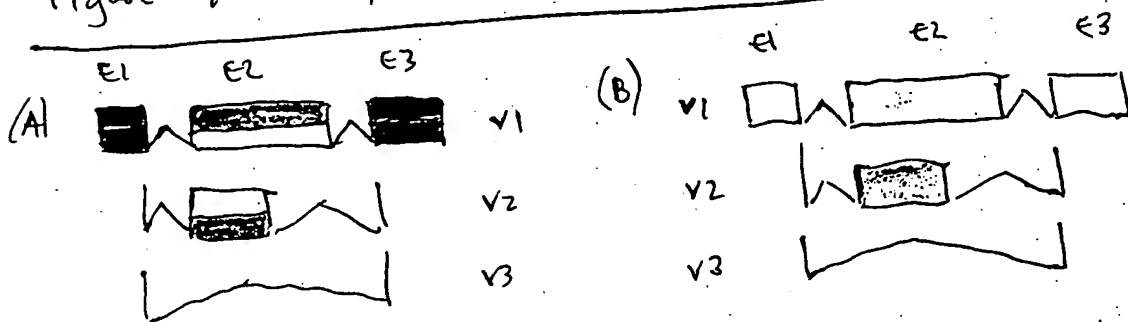


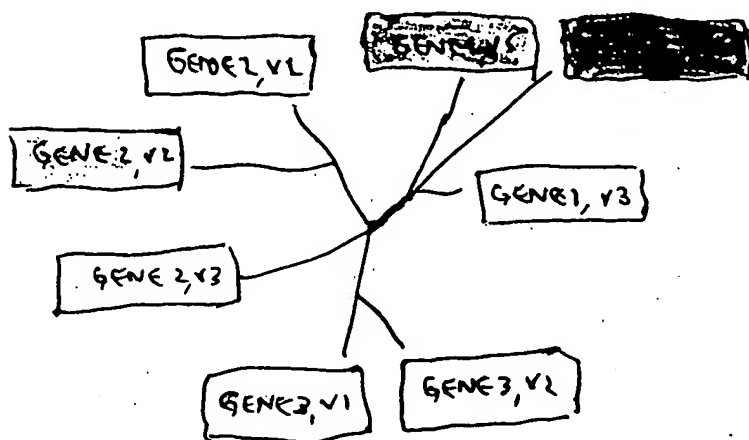
Figure 19 Expression from Two samples



The bar representing each exon is split in half, with each half used to display the expression level of one sample. In this example, V_1 of exon 2 (E_2) is more highly expressed in sample one (the top half of the bar), while variant two (V_2) of exon 2 is more highly expressed in sample two (the bottom half of the bar). Exons 1 and 3 are equally expressed in both samples.

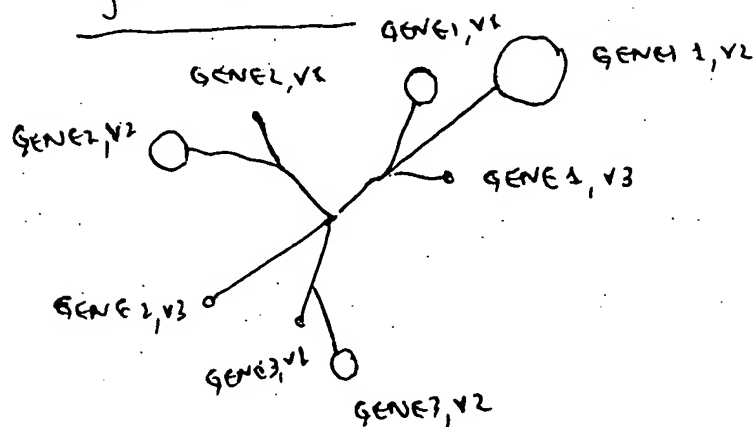
Samples one and two are shown in different colors. Exon 2 (E_2) is differentially expressed. In sample one (green), variant one (V_1) is more highly expressed. In sample two (red), variant two (V_2) is more highly expressed. Exons one and three (E_1 & E_3) are equally expressed in the two samples (indicated with white).

Figure 20(A) Expression levels in cluster Views



A hypothetical hierarchical cluster of three genes (GENE1, GENE2 and GENE3) and their variants. Each node has a rectangular label. The label's color saturation indicates the expression level. In this example, gene two variants one and three are not expressed (indicated with white), while gene two variant two (GENE2, v2) is expressed (indicated with gray). Gene one, variant two is expressed more highly than variant one (indicated with a darker, more saturated gray).

Figure 20 (B)

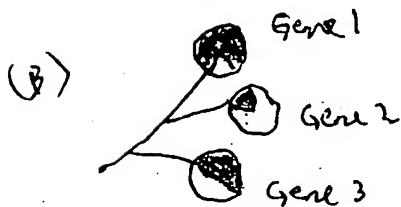


Relative expression levels are indicated by the size of the circle shown at each node.

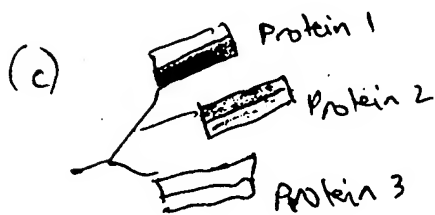
Figure 21 Clusters and Expression in Two Samples



Gene one is more highly expressed in sample two (shown in red), gene two is more highly expressed in sample one (indicated with green), while gene 3 is equally expressed in the two samples.



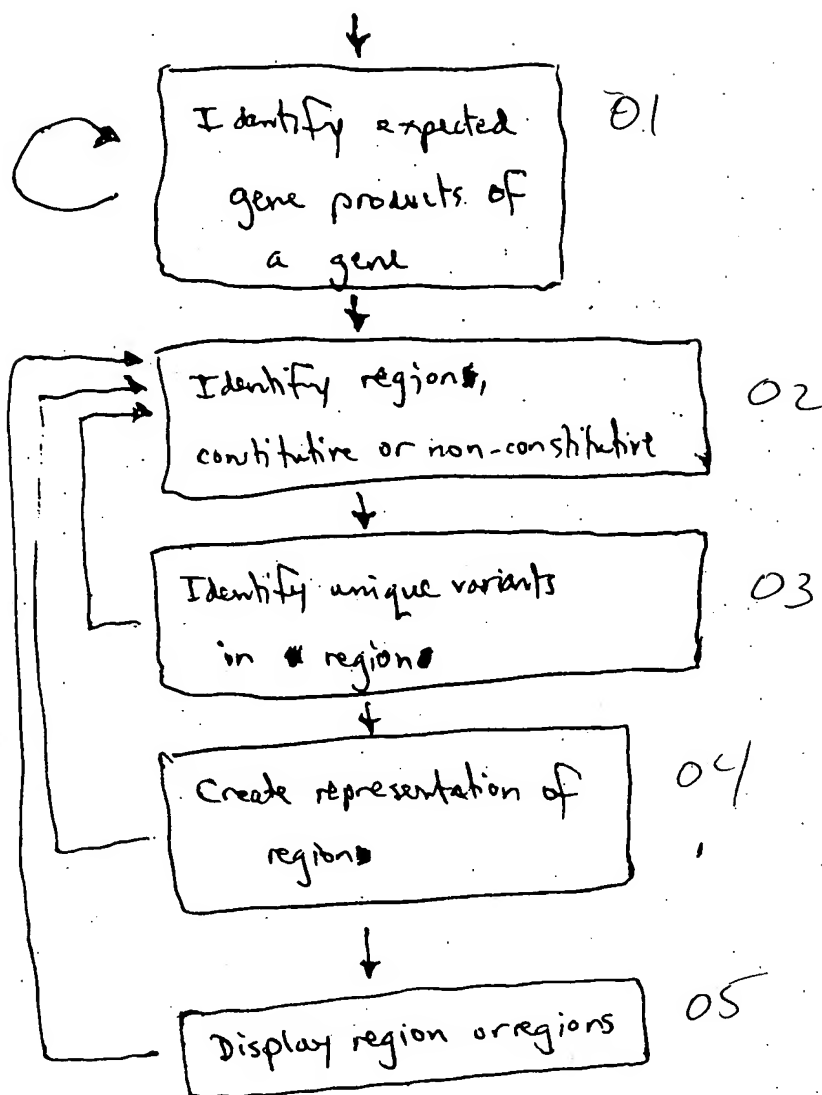
Portions of the display area are allocated to indicate relative expression, such as the ratio between two samples.



The display area for each protein is split. In each portion, expression in one sample is shown with a color and a saturation. Protein 3 is not expressed in either sample; protein 1 more highly in sample 2 (red); and protein 2, more highly in sample one (green).

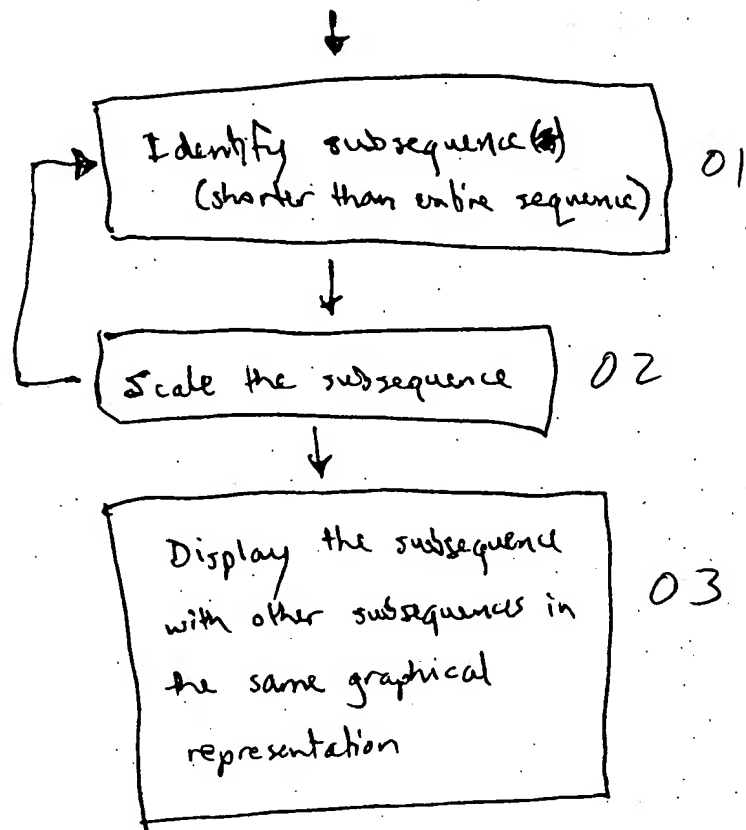
Flow chart 1

Fig 22



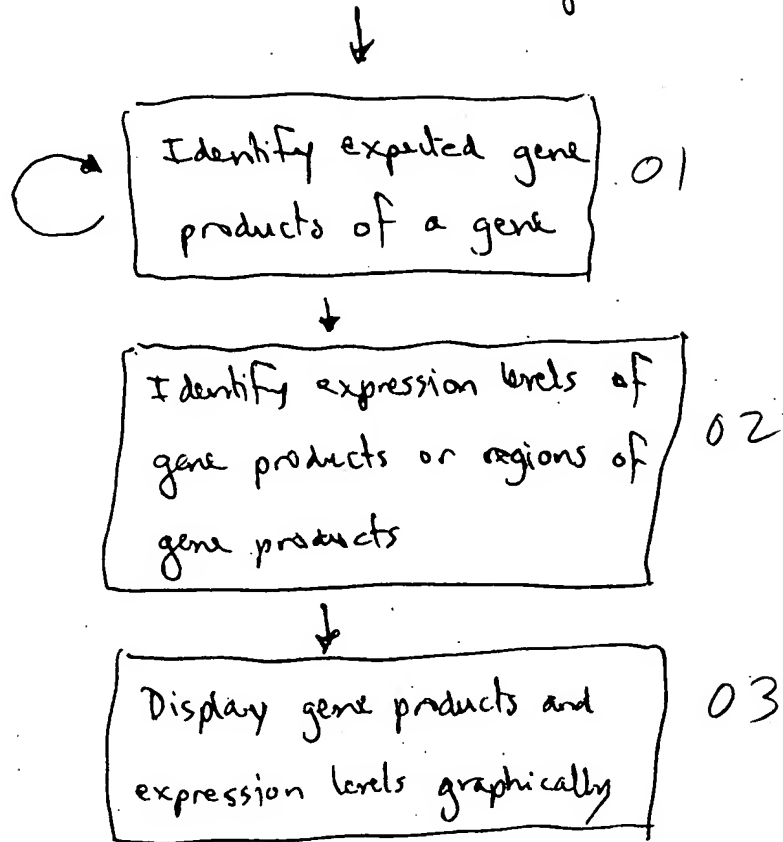
Flow Chart 23

Fig 22 23



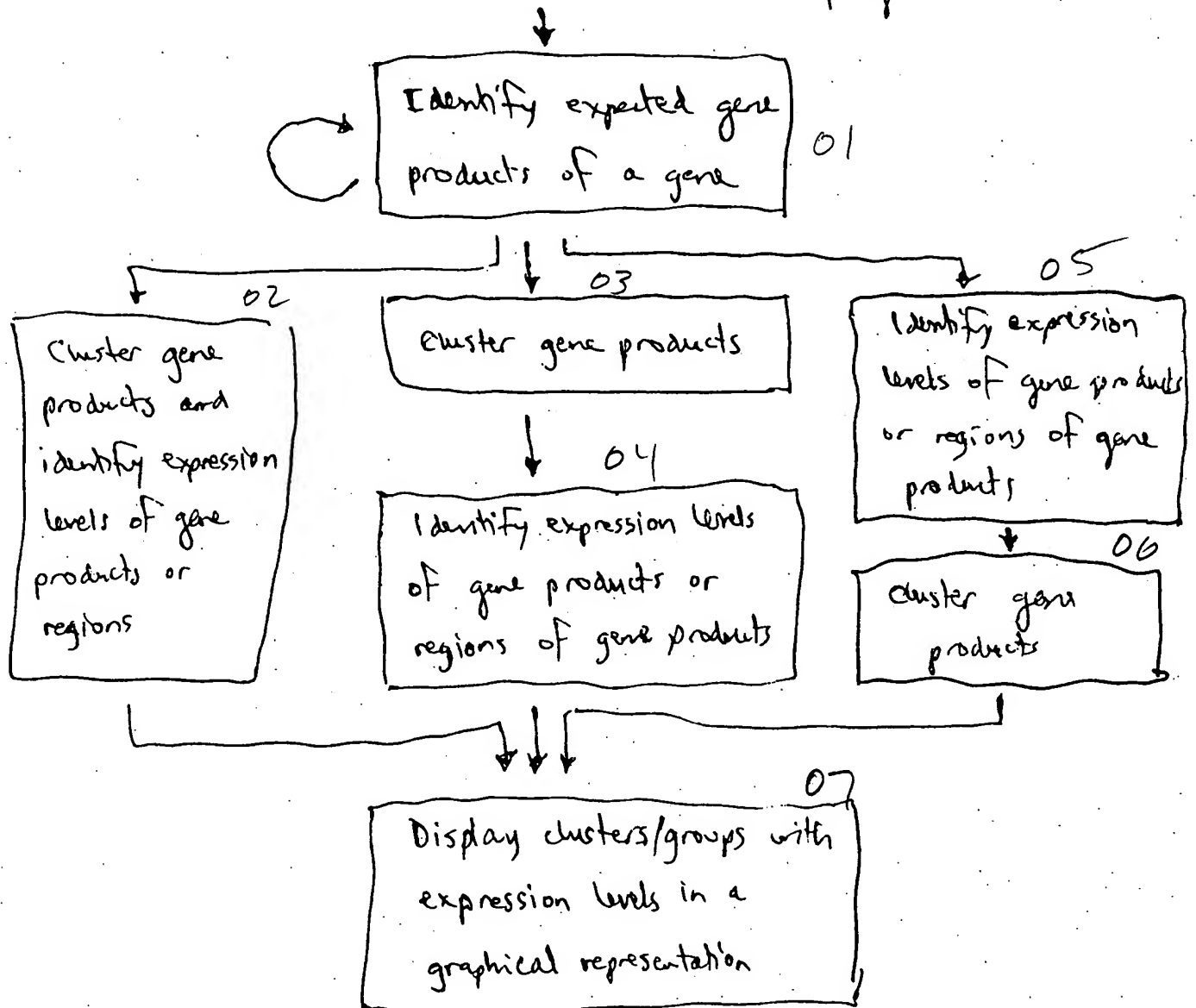
Flow chart 3

Fig 24



Flow chart 4

Fig 25



Flow chart 5

Fig 24

